

5620

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/519,447
Source: PCT
Date Processed by STIC: 1-12-05

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PCT

RAW SEQUENCE LISTING DATE: 01/12/2005
PATENT APPLICATION: US/10/519,447 TIME: 16:15:44

Input Set : A:\Q85576 Sequence Listing.txt
Output Set: N:\CRF4\01122005\J519447.raw

3 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
4 Makoto OGINO
5 Hideki ENDOH
7 <120> TITLE OF INVENTION: METHOD FOR SCREENING AN AGENT FOR IMPROVING INSULIN
RESISTANCE
9 <130> FILE REFERENCE: Q85576
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/519,447
C--> 11 <141> CURRENT FILING DATE: 2004-12-30
11 <150> PRIOR APPLICATION NUMBER: PCT/JP03/08367
12 <151> PRIOR FILING DATE: 2003-07-01
14 <150> PRIOR APPLICATION NUMBER: JP 2002-193814
15 <151> PRIOR FILING DATE: 2002-07-02
17 <160> NUMBER OF SEQ ID NOS: 16
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1845
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(1845)
29 <223> OTHER INFORMATION:
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34 Met Ser Gly Tyr Ser Ser Asp Arg Asp Arg Gly Arg Asp Arg Gly Phe
35 1 5 . 10 15
37 ggt gca cct cga ttt gga gga agt agg gca ggg ccc tta tct gga aag 96
38 Gly Ala Pro Arg Phe Gly Gly Ser Arg Ala Gly Pro Leu Ser Gly Lys
39 20 25 30
41 aag ttt gga aac cct ggg gag aaa tta gtt aaa aag aag tgg aat ctt 144
42 Lys Phe Gly Asn Pro Gly Glu Lys Leu Val Lys Lys Trp Asn Leu
43 35 40 45
45 gat gag ctg cct aaa ttt gag aag aat ttt tat caa gag cac cct gat 192
46 Asp Glu Leu Pro Lys Phe Glu Lys Asn Phe Tyr Gln Glu His Pro Asp
47 50 55 . 60
49 ttg gct agg cgc aca gca caa gag gtg gaa aca tac aga aga agc aag 240
50 Leu Ala Arg Arg Thr Ala Gln Glu Val Glu Thr Tyr Arg Arg Ser Lys
51 65 70 75 80
53 gaa att aca gtt aga ggt cac aac tgc ccg aag cca gtt cta aat ttt 288
54 Glu Ile Thr Val Arg Gly His Asn Cys Pro Lys Pro Val Leu Asn Phe
55 85 90 95
57 tat gaa gcc aat ttc cct gca aat gtc atg gat gtt att gca aga cag 336
58 Tyr Glu Ala Asn Phe Pro Ala Asn Val Met Asp Val Ile Ala Arg Gln
59 100 105 110

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61	aat ttc act gaa ccc act gct att caa gct cag gga tgg cca gtt gct	384
62	Asn Phe Thr Glu Pro Thr Ala Ile Gln Ala Gln Gly Trp Pro Val Ala	---
63	115 120 125	
65	cta agt gga ttg gat atg gtt gga gtg gca cag act gga tct ggg aaa	432
66	Leu Ser Gly Leu Asp Met Val Gly Val Ala Gln Thr Gly Ser Gly Lys	
67	130 135 140	
69	aca ttg tct tat ttg ctt cct gcc att gtc cac atc aat cat cag cca	480
70	Thr Leu Ser Tyr Leu Leu Pro Ala Ile Val His Ile Asn His Gln Pro	
71	145 150 155 160	
73	tcc cta gag aga ggc gat ggg cct att tgt ttg gtg ctg gca cca act	528
74	Phe Leu Glu Arg Gly Asp Gly Pro Ile Cys Leu Val Leu Ala Pro Thr	
75	165 170 175	
77	cgg gaa ctg gcc caa cag gtg cag caa gta gct gct gaa tat tgt aga	576
78	Arg Glu Leu Ala Gln Gln Val Gln Gln Val Ala Ala Glu Tyr Cys Arg	
79	180 185 190	
81	gca tgt cgc ttg aag tct act tgt atc tac ggt ggt gct cct aag gga	624
82	Ala Cys Arg Leu Lys Ser Thr Cys Ile Tyr Gly Ala Pro Lys Gly	
83	195 200 205	
85	cca caa ata cgt gat ttg gag aga ggt gtg gaa atc tgt att gca aca	672
86	Pro Gln Ile Arg Asp Leu Glu Arg Gly Val Glu Ile Cys Ile Ala Thr	
87	210 215 220	
89	cct gga aga ctg att gac ttt tta gag tgt gga aaa acc aat ctg aga	720
90	Pro Gly Arg Leu Ile Asp Phe Leu Glu Cys Gly Lys Thr Asn Leu Arg	
91	225 230 235 240	
93	aga aca acc tac ctt gtc ctt gat gaa gca gat aga atg ctt gat atg	768
94	Arg Thr Thr Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp Met	
95	245 250 255	
97	ggc ttt gaa ccc caa ata agg aag att gtg gat caa ata aga cct gat	816
98	Gly Phe Glu Pro Gln Ile Arg Lys Ile Val Asp Gln Ile Arg Pro Asp	
99	260 265 270	
101	agg caa act cta atg tgg agt gcg act tgg cca aaa gaa gta aga cag	864
102	Arg Gln Thr Leu Met Trp Ser Ala Thr Trp Pro Lys Glu Val Arg Gln	
103	275 280 285	
105	ctt gct gaa gat ttc ctg aaa gac tat att cat ata aac att ggt gca	912
106	Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile His Ile Asn Ile Gly Ala	
107	290 295 300	
109	ctt gaa ctg agt gca aac cac aac att ctt cag att gtg gat gtg tgt	960
110	Leu Glu Leu Ser Ala Asn His Asn Ile Leu Gln Ile Val Asp Val Cys	
111	305 310 315 320	
113	cat gac gta gaa aag gat gaa aaa ctt att cgt cta atg gaa gag atc	1008
114	His Asp Val Glu Lys Asp Glu Lys Leu Ile Arg Leu Met Glu Glu Ile	
115	325 330 335	
117	atg agt gag aag gag aat aaa acc att gtt ttt gtg gaa acc aaa aga	1056
118	Met Ser Glu Lys Glu Asn Lys Thr Ile Val Phe Val Glu Thr Lys Arg	
119	340 345 350	
121	aga tgt gat gag ctt acc aga aaa atg agg aga gat ggg tgg cct gcc	1104
122	Arg Cys Asp Glu Leu Thr Arg Lys Met Arg Arg Asp Gly Trp Pro Ala	
123	355 360 365	
125	atg ggt atc cat ggt gac aag agt caa gag cgt gac tgg gtt cta	1152

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126 Met Gly Ile His Gly Asp Lys Ser Gln Gln Glu Arg Asp Trp Val Leu		
127 370	--375--	380
129 aat gaa ttc aaa cat gga aaa gct cct att ctg att gct aca gat gtg		1200
130 Asn Glu Phe Lys His Gly Lys Ala Pro Ile Leu Ile Ala Thr Asp Val		
131 385	390	395 400
133 gcc tcc aga ggg cta gat gtg gaa gat gtg aaa ttt gtc atc aat tat		1248
134 Ala Ser Arg Gly Leu Asp Val Glu Asp Val Lys Phe Val Ile Asn Tyr		
135 405	410	415
137 gac tac cct aac tcc tca gag gat tat att cat cga att gga aga act		1296
138 Asp Tyr Pro Asn Ser Ser Glu Asp Tyr Ile His Arg Ile Gly Arg Thr		
139 420	425	430
141 gct cgc agt acc aaa aca ggc aca gca tac act ttc ttt aca cct aat		1344
142 Ala Arg Ser Thr Lys Thr Gly Thr Ala Tyr Thr Phe Thr Pro Asn		
143 435	440	445
145 aac ata aag caa gtg agc gac ctt atc tct gtg ctt cgt gaa gct aat		1392
146 Asn Ile Lys Gln Val Ser Asp Leu Ile Ser Val Leu Arg Glu Ala Asn		
147 450	455	460
149 caa gca att aat ccc aag ttg ctt cag ttg gtc gaa gac aga ggt tca		1440
150 Gln Ala Ile Asn Pro Lys Leu Leu Gln Leu Val Glu Asp Arg Gly Ser		
151 465	470	475 480
153 ggt cgt tcc agg ggt aga gga ggc atg aag gat gac cgt cgg gac aga		1488
154 Gly Arg Ser Arg Gly Arg Gly Gly Met Lys Asp Asp Arg Arg Asp Arg		
155 485	490	495
157 tac tct gcg ggc aaa agg ggt gga ttt aat acc ttt aga gac agg gaa		1536
158 Tyr Ser Ala Gly Lys Arg Gly Gly Phe Asn Thr Phe Arg Asp Arg Glu		
159 500	505	510
161 aat tat gac aga ggt tac tct agc ctg ctt aaa aga gat ttt ggg gca		1584
162 Asn Tyr Asp Arg Gly Tyr Ser Ser Leu Leu Lys Arg Asp Phe Gly Ala		
163 515	520	525
165 aaa act cag aat ggt gtt tac agt gct gca aat tac acc aat ggg agc		1632
166 Lys Thr Gln Asn Gly Val Tyr Ser Ala Ala Asn Tyr Thr Asn Gly Ser		
167 530	535	540
169 ttt gga agt aat ttt gtg tct gct ggt ata cag acc agt ttt agg act		1680
170 Phe Gly Ser Asn Phe Val Ser Ala Gly Ile Gln Thr Ser Phe Arg Thr		
171 545	550	555 560
173 ggt aat cca aca ggg act tac cag aat ggt tat gat agc act cag caa		1728
174 Gly Asn Pro Thr Gly Thr Tyr Gln Asn Gly Tyr Asp Ser Thr Gln Gln		
175 565	570	575
177 tac gga agt aat gtt cca aat atg cac aat ggt atg aac caa cag gca		1776
178 Tyr Gly Ser Asn Val Pro Asn Met His Asn Gly Met Asn Gln Gln Ala		
179 580	585	590
181 tat gca tat cct gct act gca gct gca cct atg att ggt tat cca atg		1824
182 Tyr Ala Tyr Pro Ala Thr Ala Ala Pro Met Ile Gly Tyr Pro Met		
183 595	600	605
185 cca aca gga tat tcc caa taa		1845
186 Pro Thr Gly Tyr Ser Gln		
187 610		
190 <210> SEQ ID NO: 2		
191 <211> LENGTH: 614		

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192 <212> TYPE: PRT
193 <213> ORGANISM: Homo sapiens —
195 <400> SEQUENCE: 2
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201 Gly Ala Pro Arg Phe Gly Gly Ser Arg Ala Gly Pro Leu Ser Gly Lys
202 20 25 30
205 Lys Phe Gly Asn Pro Gly Glu Lys Leu Val Lys Lys Trp Asn Leu
206 35 40 45
209 Asp Glu Leu Pro Lys Phe Glu Lys Asn Phe Tyr Gln Glu His Pro Asp
210 50 55 60
213 Leu Ala Arg Arg Thr Ala Gln Glu Val Glu Thr Tyr Arg Arg Ser Lys
214 65 70 75 80
217 Glu Ile Thr Val Arg Gly His Asn Cys Pro Lys Pro Val Leu Asn Phe
218 85 90 95
221 Tyr Glu Ala Asn Phe Pro Ala Asn Val Met Asp Val Ile Ala Arg Gln
222 100 105 110
225 Asn Phe Thr Glu Pro Thr Ala Ile Gln Ala Gln Gly Trp Pro Val Ala
226 115 120 125
229 Leu Ser Gly Leu Asp Met Val Gly Val Ala Gln Thr Gly Ser Gly Lys
230 130 135 140
233 Thr Leu Ser Tyr Leu Leu Pro Ala Ile Val His Ile Asn His Gln Pro
234 145 150 155 160
237 Phe Leu Glu Arg Gly Asp Gly Pro Ile Cys Leu Val Leu Ala Pro Thr
238 165 170 175
241 Arg Glu Leu Ala Gln Gln Val Gln Gln Val Ala Ala Glu Tyr Cys Arg
242 180 185 190
245 Ala Cys Arg Leu Lys Ser Thr Cys Ile Tyr Gly Gly Ala Pro Lys Gly
246 195 200 205
249 Pro Gln Ile Arg Asp Leu Glu Arg Gly Val Glu Ile Cys Ile Ala Thr
250 210 215 220
253 Pro Gly Arg Leu Ile Asp Phe Leu Glu Cys Gly Lys Thr Asn Leu Arg
254 225 230 235 240
257 Arg Thr Thr Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp Met
258 245 250 255
261 Gly Phe Glu Pro Gln Ile Arg Lys Ile Val Asp Gln Ile Arg Pro Asp
262 260 265 270
265 Arg Gln Thr Leu Met Trp Ser Ala Thr Trp Pro Lys Glu Val Arg Gln
266 275 280 285
269 Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile His Ile Asn Ile Gly Ala
270 290 295 300
273 Leu Glu Leu Ser Ala Asn His Asn Ile Leu Gln Ile Val Asp Val Cys
274 305 310 315 320
277 His Asp Val Glu Lys Asp Glu Lys Leu Ile Arg Leu Met Glu Glu Ile
278 325 330 335
281 Met Ser Glu Lys Glu Asn Lys Thr Ile Val Phe Val Glu Thr Lys Arg
282 340 345 350
285 Arg Cys Asp Glu Leu Thr Arg Lys Met Arg Arg Asp Gly Trp Pro Ala
286 355 360 365

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289	Met	Gly	Ile	His	Gly	Asp	Lys	Ser	Gln	Glu	Arg	Asp	Trp	Val	Leu	
290	370				375	--				380						
293	Asn	Glu	Phe	Lys	His	Gly	Lys	Ala	Pro	Ile	Leu	Ile	Ala	Thr	Asp	Val
294	385				390				395						400	
297	Ala	Ser	Arg	Gly	Leu	Asp	Val	Glu	Asp	Val	Lys	Phe	Val	Ile	Asn	Tyr
298					405				410						415	
301	Asp	Tyr	Pro	Asn	Ser	Ser	Glu	Asp	Tyr	Ile	His	Arg	Ile	Gly	Arg	Thr
302					420				425						430	
305	Ala	Arg	Ser	Thr	Lys	Thr	Gly	Thr	Ala	Tyr	Thr	Phe	Phe	Thr	Pro	Asn
306					435				440						445	
309	Asn	Ile	Lys	Gln	Val	Ser	Asp	Leu	Ile	Ser	Val	Leu	Arg	Glu	Ala	Asn
310					450				455						460	
313	Gln	Ala	Ile	Asn	Pro	Lys	Leu	Leu	Gln	Leu	Val	Glu	Asp	Arg	Gly	Ser
314	465					470				475						480
317	Gly	Arg	Ser	Arg	Gly	Arg	Gly	Gly	Met	Lys	Asp	Asp	Arg	Arg	Asp	Arg
318					485				490						495	
321	Tyr	Ser	Ala	Gly	Lys	Arg	Gly	Gly	Phe	Asn	Thr	Phe	Arg	Asp	Arg	Glu
322					500				505						510	
325	Asn	Tyr	Asp	Arg	Gly	Tyr	Ser	Ser	Leu	Leu	Lys	Arg	Asp	Phe	Gly	Ala
326					515				520						525	
329	Lys	Thr	Gln	Asn	Gly	Val	Tyr	Ser	Ala	Ala	Asn	Tyr	Thr	Asn	Gly	Ser
330					530				535						540	
333	Phe	Gly	Ser	Asn	Phe	Val	Ser	Ala	Gly	Ile	Gln	Thr	Ser	Phe	Arg	Thr
334					545				550						560	
337	Gly	Asn	Pro	Thr	Gly	Thr	Tyr	Gln	Asn	Gly	Tyr	Asp	Ser	Thr	Gln	Gln
338						565				570					575	
341	Tyr	Gly	Ser	Asn	Val	Pro	Asn	Met	His	Asn	Gly	Met	Asn	Gln	Gln	Ala
342					580				585						590	
345	Tyr	Ala	Tyr	Pro	Ala	Ala	Ala	Pro	Met	Ile	Gly	Tyr	Pro	Met		
346					595				600						605	
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353	<210>	SEQ	ID	NO:	3											
354	<211>	LENGTH:	1518													
355	<212>	TYPE:	DNA													
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359	<221>	NAME/KEY:	CDS													
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366	1				5					10					15	
368	ttc	act	gat	aca	ctg	tct	gca	aac	ata	tca	caa	gaa	atg	acc	atg	gtt
369	Phe	Thr	Asp	Thr	Leu	Ser	Ala	Asn	Ile	Ser	Gln	Glu	Met	Thr	Met	Val
370					20				25						30	
372	gac	aca	gag	atg	cca	ttc	tgg	ccc	acc	aac	ttt	ggg	atc	agc	tcc	gtg
373	Asp	Thr	Glu	Met	Pro	Phe	Trp	Pro	Thr	Asn	Phe	Gly	Ile	Ser	Ser	Val

VERIFICATION SUMMARY
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Input Set : A:\Q85576 Sequence Listing.txt
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:29
L:363 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:361
L:638 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:636